## SEQUENCE LISTING

	(110)	DASI AKCIENGESETISCHATC	
10	<120>	Malate dehydrogenase as target for herbicides	
15	<130>	PF 0000 054200	
	<160>	12	
20	<170>	PatentIn version 3.1	
25	<210>	1	
	<211>	673	
	<212>	DNA	
30	<213>	Nicotiana tabacum	
35	<400> gcggcc	1 gcta aacctccttg ttcttttacg ccagaggaag ctgaatattt aacatctcgt	60
	atacaa	aatg ggggaactga agttgttgag gcaaaagctg gtgctggttc ggcaactctc	120
40	tctatg	gcat atgctgcggt taaatttgcc gacgcatgtt tgcatggatt gagaggagat	180
	gctggc	attg tagaatgtgc ctttgtgtct tctcaggtga ctgaacttcc atttttcgca	240
45	tcaaaa	gtat ggcttggccg caacggagtt gaagaaatat acccccttgg tcccctaaat	300
	gaatac	gaga ggtctgggct tgagaaggca aggaaagagt tggcaacaag tgttcagaag	360
	ggtgtc	aact ttgtaaagaa atgagcagac agctacatga cttccaaaag atgcttttat	420
50	gtgggc	tata tatctcaaat ccgcagttcc agaaaataag agtagtttct ttcttgtatt	480
	äaaggg	caaa tootgttota attttotata gattgatgoo ttggtgoaga aaataaatgt	540
55	actatt	tggt catctaaaat aacaacagtc cccagtgcat gttggacttg caaagtatta	600
	catcct	ttga agcaagggct tgttatggac tttttgacag tatggatatt taaagggctt	660
	ggagag	egge ege	673
60	<210>	2	
	<211>	1505	

<212> DNA <213> Nicotiana tabacum 5 <220> <221> CDS 10 <222> (148)..(1221)<223> 15 <400> 60 ctaatacgac tcactatagg gcaagcagtg gtatcaacgc agagtacgcg ggggggaaac 20 aaaattcaat tacttacctt gatttctact acctctcttt ctcatcataa ttcaaacaca 120 caaattctca agcccaagtc ttagaat atg cag aac ggt gca gag acc tat cga 174 Met Gln Asn Gly Ala Glu Thr Tyr Arg 25 cga atg gcc acc atc tca gct cac ctt aac ccc tct cct tct tct cat 222 Arg Met Ala Thr Ile Ser Ala His Leu Asn Pro Ser Pro Ser Ser His 10 15 20 30 cag atg gag gga ggt gtg ggt ttg agc cga gct aat tgc agg gcg aaa 270 Gln Met Glu Gly Gly Val Gly Leu Ser Arg Ala Asn Cys Arg Ala Lys ggg ggt tot coa gga tto aaa gto gcg ato ttg ggt gct gca gga ggt 318 35 Gly Gly Ser Pro Gly Phe Lys Val Ala Ile Leu Gly Ala Ala Gly Gly 50 att ggt cag cca ctt gct atg ctt atg aaa acg aat cca ctg gtt tca 366 Ile Gly Gln Pro Leu Ala Met Leu Met Lys Thr Asn Pro Leu Val Ser 40 60 gtt ctg cat ctt tat gat gtt gcc aat act cct ggt gta act gct gac 414 Val Leu His Leu Tyr Asp Val Ala Asn Thr Pro Gly Val Thr Ala Asp 45 462 att agc cac atg gac act ggt gcc gtg gta cgt ggt ttt cta ggg cct Ile Ser His Met Asp Thr Gly Ala Val Val Arg Gly Phe Leu Gly Pro 100 50 caa caa ttg gaa gat gct ctc act ggc atg gac ctt gta ata atc cct 510 Gln Gln Leu Glu Asp Ala Leu Thr Gly Met Asp Leu Val Ile Ile Pro-110 115 558 gct ggt gtt cct aga aaa cca ggc atg aca aga gat gat ctt ttc aac Ala Gly Val Pro Arg Lys Pro Gly Met Thr Arg Asp Asp Leu Phe Asn 130 atc aat gca gga att gtg agg act tta tgt gaa gga att gcc aag tgc 606 Ile Asn Ala Gly Ile Val Arg Thr Leu Cys Glu Gly Ile Ala Lys Cys 60 145 tgt cct aag gcc att gtt aac ata att agt aat cct gtt aac tct aca 654 Cys Pro Lys Ala Ile Val Asn Ile Ile Ser Asn Pro Val Asn Ser Thr 160 165

5		cca Pro															702
		aga Arg	-	_				_		_		_	_	_			750
10		gtg Val	_	_	_	_			-			-		_	_		798
15		gtg Val															846
20		aaa Lys 235															894
25		cgt Arg							_	_	_		-		_		942
20	•	ggt Gly	-	-				_			-	-	_			_	990
30	-	gca Ala	_	_			-	-		_	_			_	_	_	1038
35		ttt Phe															1086
40		cgg Arg 315															1134
45		aat Asn															1182
-10		aca Thr												tga	gcag	aca	1231
50	gct	acat	gac	ttcc	aaaa	ga t	gctt	ttat	g tg	ggct	atat	atc	tcaa	atc (	cgca	gttcca	a 1291
	gaa	aata	aga	gtag	tttc	tt t	cttg	tatt	a aa	gggc	aaat	cct	gttc	taa '	tttt	ctata	g 1351
55	att	gatg	cct	tggt	gcag	aa a	ataa	atgt	a ct	attt	ggtc	atc	taaa	ata .	acaa	cagtc	c 1411
JJ	cca	gtgc	atg	ttgg	actt	gc a	aagt	atta	c at	cctt	tgaa	gca	aggg	ctt	gtta	tggac	1471
	ttt	tgac	agt .	atgg	atat	tt a	aagg	gctt	g ga	ga			•			• •	1505
60																	

<210> 3

<211> 358

<2	1	2	PRT
<b>~</b> ∠	1	~~	FRI

.cotiana	tabacum
	cotiana

	٩	

<400> 3

- Met Gln Asn Gly Ala Glu Thr Tyr Arg Arg Met Ala Thr Ile Ser Ala

  10 1 5 10 15
- His Leu Asn Pro Ser Pro Ser Ser His Gln Met Glu Gly Gly Val Gly 20 25 30
  - Leu Ser Arg Ala Asn Cys Arg Ala Lys Gly Gly Ser Pro Gly Phe Lys 35 40 45
- Val Ala Ile Leu Gly Ala Ala Gly Gly Ile Gly Gln Pro Leu Ala Met
  50 55 60
- Leu Met Lys Thr Asn Pro Leu Val Ser Val Leu His Leu Tyr Asp Val 65 70 75 80
- Ala Asn Thr Pro Gly Val Thr Ala Asp Ile Ser His Met Asp Thr Gly 30 85 90 95
- Ala Val Val Arg Gly Phe Leu Gly Pro Gln Gln Leu Glu Asp Ala Leu
  100 105 110
  - Thr Gly Met Asp Leu Val Ile Ile Pro Ala Gly Val Pro Arg Lys Pro 115 120 125
- Gly Met Thr Arg Asp Asp Leu Phe Asn Ile Asn Ala Gly Ile Val Arg
  130 135 140
- Thr Leu Cys Glu Gly Ile Ala Lys Cys Cys Pro Lys Ala Ile Val Asn 145 150 155 160
- Ile Ile Ser Asn Pro Val Asn Ser Thr Val Pro Ile Ala Ala Glu Val 165 170 175
- Phe Lys Lys Ala Gly Thr Phe Asp Pro Arg Arg Leu Leu Gly Val Thr
  180 185 190
  - Met Leu Asp Ile Val Arg Ala Asn Thr Phe Val Ala Glu Val Leu Gly
    . 195 200 205
- 60
  Leu Asp Pro Arg Glu Val Asp Val Pro Val Val Gly Gly His Ala Gly 210 215 220

**5** 

	225	Int	iie	reu	PIO	230	Leu	ser	GIN	vaı	235	PIO	PIO	Cys	Ser	240	
5	Thr	Pro	Glu	Glu	Thr 245	Glu	Tyr	Leu	Thr	Ser 250	Arg	Ile	Gln	Asn	Gly 255	Gly	
10	Thr	Glu	Val	Val 260	Glu	Ala	Lys	Ala	Gly 265	Ala	Gly	Ser	Ala	Thr 270	Leu	Ser	
15	Met	Ala	Tyr 275	Ala	Ala	Val	Lys	Phe 280	Ala	Asp	Ala	Cys	Leu 285	His	Gly	Leu	
20	Arg	Gly 290	Asp	Ala	Gly	Ile	Val 295	Glu	Суѕ	Ala	Phe	Val 300	Ser	Ser	Gln	Val	
20	Thr 305	Glu	Leu	Pro	Phe	Phe 310	Ala	Ser	Lys	Val	Arg 315	Leu	Gly	Arg	Asn	Gly 320	
25	Val	Glu	Glu	Ile	Tyr 325	Pro	Leu	Gly	Pro	Leu 330	Asn	Glu	Tyr	Glu	Arg 335	Ser	
30	Gly	Leu	Glu	Lys 340	Ala	Lys	Lys	Glu	Leu 345	Ala	Thr	Ser	Val	Gln 350	Lys	Gly	
35	Val	Asn	Phe 355	Val	Lys	Lys											
	<210	0>	4														•
40	<21	1>	16														
	<212	2>	DNA														
	<21	3> :	Arti:	fici	al S	eque	nce										
45																	
	<220	0>															
50	<223	3>	Prime	er													
	<400 agaa		4 gcg (	gccg	ct												16
55	<21	0>	5														
	<21	1>	32														
60	<21	2>	DNA														
00	<21	3>	Arti	fici	al S	eque	nce										

<210> 9

6`

	<220>		
	<223>	Primer	
	<400> ctcatgo	5 egge egegegeaac geaattaatg tg	32
10	<210>	6	
	<211>	32	
	<212>	DNA	
15	<213>	Artificial Sequence	
20	<220>		
20	<223>	Primer	
25	<400> tcatgco	6 ggcc gcgagatcca gttcgatgta ac	32
	<210>	7	
20	<211>	21	
30	<212>	DNA	
	<213>	Artificial Sequence	
35			
	<220>		
40	<223>	Primer	
40	<400> gtggat	7 tgat gtgatatctc c	21
45	<210>	8	
	<211>	21	
<b>50</b>	<212,>	DNA	
50	<213>	Artificial Sequence	
55	<220>		
	<223>	Primer	
60	<400> gtaagg	8 atct gagctacaca t	21

		7	
	<211>	17	
	<212>	DNA	
5	<213>	Artificial Sequence	
		•	
10	<220>	·	
10	<223>	Primer	
15	<400> atgagg	9 gcga aaggggg	17
	<210>	10	
20	<211>	25	
20	<212>	DNA ·	
	<213>	Artificial Sequence	
25			
	<220>		
30	<223>	Primer	
00	<400> tttctt	10 taca aagttgacac ccttc	25
35	<210>	11	
	<211>	17	
40	<212>	DNA	
40	<213>	Artificial Sequence	
45	<220>		
	<223>	Primer	
50	<400> atgcgg	11 ggcaa aaggtgg	17
	<210>	12	
55	<211>		
	<212>		
		Artificial Sequence	
60			
	<220>		

8

<223> Primer

<400> 12 tttcttcgca aaggtaacac c

tttcttcgca aaggtaacac c
5

21